



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 170748

TO: Ulrike Winkler
Location: REM-3A39&3C18
Art Unit: 1648
Monday, November 07, 2005

Case Serial Number: 09/856086

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Winkler,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

170748

From: Winkler, Ulrike
Sent: Friday, November 04, 2005 1:09 PM
To: STIC-Biotech/ChemLib

STIC,

Please search SEQ ID NO:8 from application # 09/856086.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
Patent Examiner, Art Unit 1648
Remsen 3A39 / Mail Box 3C18
tel. 571-272-0912
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CHFE

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 11/7/05
Date completed: 11/7/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 11:38:38 ; Search time 170 Seconds
(without alignments)
20.476 Million cell updates/sec

Title: US-09-856-086b-8
Perfect score: 49
Sequence: 1 ISRFAMGEV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	2 AAW56752	Aaw56752 A. calcoa
2	49	100.0	9	2 AAY42322	Aay42322 Acinetoba
3	49	100.0	9	7 AAE37623	Aae37623 Acinetoba
4	49	100.0	15	7 AAE37638	Aae37638 Bovine my
5	46	93.9	141	6 ADA35940	Ada35940 Acinetoba
6	39	79.6	136	7 ABO67408	Ab067408 Klebsiell
7	39	79.6	371	6 ADB07186	Adb07186 Alloiococ
8	39	79.6	426	7 ADC94570	Adc94570 E. faeciu
9	39	79.6	445	4 AAU33514	Aau33514 Enterococ
10	39	79.6	447	4 AAU35315	Aau35315 Enterococ
11	39	79.6	447	6 ABU14587	Abu14587 Protein e
12	39	79.6	450	6 ADB07188	Adb07188 Alloiococ
13	39	79.6	459	6 ADB07190	Adb07190 Alloiococ
14	38	77.6	746	6 ADB21625	Abu21625 Protein e
15	37.5	76.5	234	7 AD808590	Ad808590 Novel pro
16	37	75.5	6	7 AAE37634	Aae37634 Bovine my
17	37	75.5	518	4 AAU40001	Aau40001 Propionib
18	37	75.5	518	6 ABM36520	Abm36520 Propionib
19	37	75.5	736	6 ABU21851	Abu21851 Protein e
20	36	73.5	156	4 AAU48680	Aau48680 Propionib
21	36	73.5	156	6 ABM45199	Abm45199 Propionib
22	36	73.5	230	8 AD014172	Ad014172 Influenza
23	36	73.5	230	8 AD014181	Ad014181 Influenza
24	36	73.5	233	8 ADL04631	Adl04631 M. catarr
25	36	73.5	300	4 ABG19523	Abg19523 Novel hum

ALIGNMENTS

RESULT 1
AAW56752

ID AAW56752 standard; peptide; 9 AA.

XX AAW56752;

XX 31-JUL-1998 (first entry)

XX A. calcoaceticus antigenic peptide exhibiting molecular mimicry.

XX BSE; bovine; myelin; molecular mimicry; antigenic; assay; diagnosis;
KW spongiform encephalopathy; Creutzfeldt Jacob disease; multiple sclerosis;
KW Acinetobacter calcoaceticus; Agrobacterium; Ruminococcus.

XX Acinetobacter calcoaceticus.

XX WO9813694-Al.

XX 02-APR-1998.

XX 29-SEP-1997; 97WO-GB002667.

XX 27-SEP-1996; 96GB-00020195.

XX (UNLO) KING'S COLLEGE.

XX Ebringer A;

XX WPI; 1998-230844/20.

XX Diagnosis of demyelinating conditions, particularly BSE - by assaying for antibodies which bind to an antigenic peptide which exhibits molecular mimicry of a mammalian myelin peptide.

XX Claim 7; Page 7; 12pp; English.

XX This is a Acinetobacter calcoaceticus antigenic peptide that exhibits molecular mimicry to a bovine myelin peptide. This is used in the methods and diagnostic tests for spongiform encephalopathy (SE) and other demyelinating conditions in mammals which comprises assaying antibodies present in the mammal which bind to an antigenic peptide which exhibits molecular mimicry of a mammalian myelin peptide. A method for testing for bovine SE (BSE) in cattle comprises assaying sera collected from the cattle for antibodies to a species of Acinetobacter, Agrobacterium or Ruminococcus, or a peptide having a sequence present in the species which mimics a peptide of bovine myelin and identifying animals having a level of antibodies at least 2 standard deviations above that of healthy control animals. The diagnostic test kit for BSE in cattle comprises as

Abg23355 Novel hum
Abm70647 Photorhab
Abp71684 C. elegans
Abbs3300 Lactococc
Abu16799 Protein e
Abr82110 Human MHC
Adq97281 Human can
Aar61853 MBP pepti
Aar61951 MBP pepti
Aar61960 MBP pepti
Aay27077 Myelin ba
Aaw94964 MHC bindi
Aae37639 Bovine my
Aar95345 MBP-3.1
Aaw3951 Human mye
Aar95394 Residues
Aar95344 MBP-3 (11
Aaw43950 Human mye
Aaw44066 Human mye
Aaw73618 Human mye

26 36 73.5 300 4 ABG23355
27 36 73.5 376 6 ABM70647
28 36 73.5 451 6 ABP71684
29 36 73.5 455 5 ABB53300
30 36 73.5 464 6 ABU16799
31 36 73.5 884 6 ABR82110
32 36 73.5 885 8 ADQ97281
33 35 71.4 9 2 AAR61853
34 35 71.4 10 2 AAR61951
35 35 71.4 11 2 AAR61960
36 35 71.4 12 2 AAY27077
37 35 71.4 13 2 AAW94964
38 35 71.4 15 7 AAE37639
39 35 71.4 19 2 AAR95345
40 35 71.4 19 2 AAW43951
41 35 71.4 20 2 AAR95394
42 35 71.4 20 2 AAW43950
43 35 71.4 20 2 AAW43950
44 35 71.4 20 2 AAW44066
45 35 71.4 20 2 AAW73618

CC test antigen a species of Acinetobacter, Ruminococcus or Agrobacterium or
 CC a peptide having a sequence present in the species which mimics a peptide
 CC of bovine myelin. The methods can be used for diagnosis of demyelinating
 CC conditions such as BSE, Creutzfeldt Jacob disease and multiple sclerosis
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
 |||||
 Db 1 ISRFAMGEV 9

RESULT 2
 AAY42322
 ID AAY42322 standard; peptide; 9 AA.

XX AAY42322;

XX 06-DEC-1999 (first entry)

XX Acinetobacter-derived peptide epitope #2.

XX Acinetobacter; myelin; spongiform encephalopathy; CJD; immune response;
 KW Creutzfeldt-Jakob disease; multiple sclerosis; antibody; epitope;
 KW detection.

XX Synthetic.

OS Acinetobacter sp.

XX WO9947932-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-GB000876.

XX 19-MAR-1998; 98GB-00005913.

XX (UNLO) UNIV LONDON KING'S COLLEGE.

XX Ebringer A;

XX WPI; 1999-571874/48.

XX Detecting de-myelinating disease or spongiform encephalopathy.

XX Claim 12; Page 7; 11pp; English.

XX This sequence represents a synthetic peptide epitope (#2) derived from
 CC species of Acinetobacter, which is sufficiently conformationally similar
 CC to natural Acinetobacter peptide epitopes to bind the corresponding
 CC antibodies. Acinetobacter species may be implicated in spongiform
 CC encephalopathies such as Creutzfeldt-Jakob disease or in de-myelinating
 CC diseases such as multiple sclerosis. Involvement of Acinetobacter forms
 CC the basis for a model for the development of de-myelinating diseases (and
 CC an alternative model for the development of spongiform encephalopathies).
 CC This model involves the phenomenon of molecular mimicry in which mammals
 CC exposed to certain bacteria containing peptide sequences which mimic
 CC myelin peptides, experience an autoimmune response. A novel method for
 CC detecting a de-myelinating disease or spongiform encephalopathy in
 CC mammals has been developed which comprises testing a biological sample
 CC obtained from the mammal for immunoglobulin A (IgA) antibodies indicative
 CC of infection by Acinetobacter species. This sequence can be used as a
 CC test antigen in a kit to detect such antibodies. The method is useful for
 CC diagnosing de-myelinating diseases and spongiform encephalopathies in
 CC animals and humans, especially bovine spongiform encephalopathy, multiple
 CC sclerosis or Creutzfeldt-Jacob disease in humans. The method is useful
 CC for the early detection of these infections, resulting in early
 CC treatments

SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
 |||||
 Db 1 ISRFAMGEV 9

RESULT 3

AAE37623
 ID AAE37623 standard; peptide; 9 AA.

XX AAE37623;

XX 27-AUG-2003 (first entry)

XX Acinetobacter sp. epitope peptide #2.

XX Demyelinating disease; spongiform encephalopathy; multiple sclerosis;
 KW Creutzfeldt-Jakob disease; CJD; bovine spongiform encephalopathy; BSE;
 KW MS; prion; epitope.

XX Acinetobacter sp.

XX WO2003040685-A2.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-GB005056.

XX 09-NOV-2001; 2001GB-00027000.

XX 04-FEB-2002; 2002GB-00002562.

XX (UNLO) KINGS COLLEGE LONDON.

XX Ebringer A, Wilson CDD;

XX WPI; 2003-441611/41.

XX Detecting demyelinating disease or spongiform encephalopathy in
 PT vertebrates, e.g. multiple sclerosis, Creutzfeldt-Jakob disease, by
 PT testing vertebrate sample for antibodies that bind to antigen in
 PT vertebrate prion.

XX Claim 19; Page 18; 50pp; English.

XX The invention relates to a method for detecting demyelinating disease or
 CC spongiform encephalopathy in vertebrates which comprises testing
 CC vertebrate sample for antibodies that bind to antigen in vertebrate
 CC prion. The invention is useful for detecting a demyelinating disease or
 CC spongiform encephalopathy in vertebrates, including bovine spongiform
 CC encephalopathy (BSE), multiple sclerosis (MS) and Creutzfeldt-Jakob
 CC disease (CJD). The present sequence is Acinetobacter sp. epitope peptide.
 CC This sequence is used to illustrate the method of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 49; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
 |||||
 Db 1 ISRFAMGEV 9

RESULT 4

AAE37638
 ID AAE37638 standard; peptide; 15 AA.

XX


```

AC AAE37638;
XX
XX
DT 27-AUG-2003 (first entry)
XX
XX DE Bovine myelin antigenic peptide #5.
XX
XX DE Demyelinating disease; spongiform encephalopathy; multiple sclerosis;
KW Creutzfeldt-Jakob disease; CJD; bovine spongiform encephalopathy; BSE;
XX MS; prion; bovine; myelin; antigen.
XX
XX OS Bos sp.
XX
XX PN WO2003040685-A2.
XX
XX PD 15-MAY-2003.
XX
XX PF 08-NOV-2002; 2002WO-GB005056.
XX
XX PR 09-NOV-2001; 2001GB-00027000.
XX
XX PR 04-FEB-2002; 2002GB-00002562.
XX
XX PA (UNLO ) KINGS COLLEGE LONDON.
XX
XX PI Ebringer A, Wilson CDD;
XX
XX DR WPI; 2003-441611/41.
XX
XX PT Detecting demyelinating disease or spongiform encephalopathy in
XX vertebrates, e.g. multiple sclerosis, Creutzfeldt-Jakob disease, by
XX testing vertebrate sample for antibodies that bind to antigen in
XX vertebrate prion.
XX
XX PS Example 3; Page 10; 50pp; English.
XX
XX CC The invention relates to a method for detecting demyelinating disease or
XX spongiform encephalopathy in vertebrates which comprises testing
XX vertebrate sample for antibodies that bind to antigen in vertebrate
XX prion. The invention is useful for detecting a demyelinating disease or
XX spongiform encephalopathy in vertebrates, including bovine spongiform
XX encephalopathy (BSE), multiple sclerosis (MS) and Creutzfeldt-Jakob
XX disease (CJD). The present sequence is bovine myelin antigenic peptide.
XX This sequence is used to illustrate the method of the invention
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 100.0%; Score 49; DB 7; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 0.064;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
Db |||||
4 ISRFAMGEV 12

RESULT 5
ADA35940
ID ADA35940 standard; protein; 141 AA.
XX
XX AC ADA35940;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Acinetobacter baumannii protein #3101.
XX
XX KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
XX plant biocontrol agent.
XX
XX OS Acinetobacter baumannii.
XX
XX PN US6562958-B1.
XX
XX PD 13-MAY-2003.
XX

PF 04-JUN-1999; 99US-00328352.
XX
XX PR 09-JUN-1998; 98US-0088701P.
XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX PI Breton G, Bush D;
XX
XX DR WPI; 2003-576092/54.
XX
XX DR N-PSDB; ADA31814.
XX
XX PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
XX PT plants.
XX
XX PS Example; SEQ ID NO 7227; 328pp; English.
XX
XX CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
XX The A. baumannii nucleic acids and polypeptides are useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX CC vaccines, as targets for antibacterial drugs, to detect the presence of
XX A. baumannii and other Acinetobacter species in a sample, in screening
XX CC compounds for the ability to interfere with the A. baumannii life cycle
XX or to inhibit A. baumannii infection, and as biocontrol agents for
XX CC plants. The present sequence represents the amino acid sequence of an A.
XX baumannii protein.
XX
XX SQ Sequence 141 AA;
XX
XX Query Match 93.9%; Score 46; DB 6; Length 141;
XX Best Local Similarity 88.9%; Pred. NO. 2.1;
XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
Db |||||
45 ISRYAMGEV 53

RESULT 6
ABO67408
ID ABO67408 standard; protein; 136 AA.
XX
XX AC ABO67408;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Klebsiella pneumoniae polypeptide seqid 13925.
XX
XX KW Recombinant expression vector; transcription regulatory element;
XX Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX OS Klebsiella pneumoniae.
XX
XX PN US6610836-B1.
XX
XX PD 26-AUG-2003.
XX
XX PF 27-JAN-2000; 2000US-00489039.
XX
XX PR 29-JAN-1999; 99US-0117747P.
XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX PI Breton GL, Osborne M;
XX
XX DR WPI; 2003-895346/82.
XX
XX DR N-PSDB; ABD00979.
XX
XX PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
XX preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX PS Disclosure; SEQ ID NO 13925; 932pp; English.

```

XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX Sequence 136 AA;

Query Match 79.6%; Score 39; DB 7; Length 136;
 Best Local Similarity 75.0%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFWNGE 8
 :|:|:|:|
 Db 48 ITRYWNGE 55

RESULT 7
 ADB07186
 ID ADB07186 standard; protein; 371 AA.
 AC ADB07186;
 XX 20-NOV-2003 (first entry)
 DT
 DE Alloicoccus otitis antigenic protein SEQ ID NO:1126.
 XX Alloicoccus otitis; antigenic protein; immunogenic; immunisation;
 KW gene therapy; Gram-positive bacterium; infection.
 XX Alloicoccus otitis.
 OS WO2003048304-A2.
 PN 12-JUN-2003.
 PD 25-NOV-2002; 2002WO-US036123.
 PF 29-NOV-2001; 2001US-0333777P.
 PR 18-NOV-2002; 2002US-0426742P.
 XX (AMHP) WYETH HOLDINGS CORP.
 PA Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;
 PI WPI; 2003-505284/47.
 DR N-PSDB; ADB07185.

XX New Alloicoccus otitis polynucleotides and polypeptides, useful for
 CC treating and diagnosing diseases, drug screening assays and monitoring of
 CC effects during drug clinical trials.
 PT Claim 33; SEQ ID NO 1126; 1019pp; English.

XX The present invention describes an isolated polynucleotide (1) of
 CC Alloicoccus otitis genomic DNA, which encodes an antigenic protein.
 CC Alloicoccus otitis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
 CC expression vector comprising the novel isolated polynucleotide (1), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against Alloicoccus otitis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying Alloicoccus
 CC otitis in the biological sample; (10) a kit comprising a container

CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (1) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting Alloicoccus
 CC otitis. The present sequence represents an Alloicoccus otitis
 CC antigen protein from the present invention.
 XX Sequence 371 AA;

Query Match 79.6%; Score 39; DB 6; Length 371;
 Best Local Similarity 85.7%; Pred. No. 97;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFWNG 7
 :|:|:|:|
 Db 188 VSRFWNG 194

RESULT 8
 ADC94570
 ID ADC94570 standard; protein; 426 AA.
 XX ADC94570;
 AC ADC94570;
 XX 01-JAN-2004 (first entry)
 DT E. faecium protein sequence SEQ ID 4197.
 XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.
 XX Enterococcus faecium.
 OS US6583275-B1.
 PN 24-JUN-2003.
 PD 30-JUN-1998; 98US-00107532.
 PF 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA Doucette-Stamm LA, Bush D;
 PI WPI; 2003-799836/75.
 DR N-PSDB; ADC90916.

XX New isolated nucleic acid derived from Enterococcus faecium encoding an
 CC Enterococcus faecium polypeptide useful for detection, prevention and
 CC treatment of a pathological condition resulting from a bacterial
 CC infection.
 PT Example 1; SEQ ID NO 4197; 243pp; English.

XX The invention relates to an isolated nucleic acid derived from
 CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC a transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids is useful for diagnosing pathological conditions
 CC resulting from E. faecium bacterial infection (e.g. urinary tract
 CC infection), bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The

CC nucleic acid is useful for recombinant production of *Candida albicans* -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating *Enterococcus faecium* infections. The present sequence represents
CC one of the disclosed *E. faecium* proteins.
XX
SQ Sequence 426 AA;

Query Match 79.6%; Score 39; DB 7; Length 426;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
:|||||
Db 241 VSRFAMG 247

RESULT 9

AAU33514

ID AAU33514 standard; protein; 445 AA.

XX

AC AAU33514;

XX 14-FEB-2002 (first entry)

XX *Enterococcus faecalis* cellular proliferation protein #150.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX *Enterococcus faecalis*.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlseen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS51373.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 5010; 51lpp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 445 AA;

Query Match 79.6%; Score 39; DB 4; Length 445;

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
:|||||
Db 262 VSRFAMG 268

RESULT 10

AAU35315

ID AAU35315 standard; protein; 447 AA.

XX

AC AAU35315;

XX 14-FEB-2002 (first entry)

XX *Enterococcus faecalis* cellular proliferation protein #602.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.

XX *Enterococcus faecalis*.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlseen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS53174.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 10908; 51lpp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 447 AA;

Query Match 79.6%; Score 39; DB 4; Length 447;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAWG 7
 :|||||
 Db 262 VSRFAWG 268

RESULT 11
 ABU14587
 ID ABU14587 standard; protein; 447 AA.
 XX
 AC ABU14587;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #114.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Enterococcus faecalis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342323P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Irawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 IN WPI; 2003.029926/02.
 DR N-PSDB; ACA18457.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 42511; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 447 AA;

Query Match 79.6%; Score 39; DB 6; Length 447;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAWG 7
 :|||||
 Db 262 VSRFAWG 268

RESULT 12
 ADB07188
 ID ADB07188 standard; protein; 450 AA.
 XX
 AC ADB07188;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Alloicoccus otitis antigenic protein SEQ ID NO:1128.
 XX
 KW Alloicoccus otitis; antigenic protein; immunogenic; immunisation;
 KW gene therapy; Gram-positive bacterium; infection.
 XX
 OS Alloicoccus otitis.
 XX
 PN WO2003048304-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 25-NOV-2002; 2002WO-US036123.
 XX
 PR 29-NOV-2001; 2001US-0333777P.
 PR 18-NOV-2002; 2002US-0426742P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;
 PI
 XX
 DR WPI; 2003-505284/47.
 DR N-PSDB; ADB07187.
 XX
 PT New Alloicoccus otitis polynucleotides and polypeptides, useful for
 PT treating and diagnosing diseases, drug screening assays and monitoring of
 PT effects during drug clinical trials.
 XX
 PS Claim 33; SEQ ID NO 1128; 1019pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (1) of
 CC Alloicoccus otitis genomic DNA, which encodes an antigenic protein.
 CC Alloicoccus otitis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
 CC expression vector comprising the novel isolated polynucleotide (1), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the

CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against *Alloiooccus* otitidis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying *Alloiooccus*
 CC otitidis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (1) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting *Alloiooccus*
 CC otitidis. The present sequence represents an *Alloiooccus* otitidis
 CC antigen protein from the present invention.

SQ Sequence 450 AA;

Query Match 79.6%; Score 39; DB 6; Length 450;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAWG 7
 :|||||
 Db 267 VSRFAWG 273

RESULT 13

ADB07190
 ID ADB07190 standard; protein; 459 AA.

AC ADB07190;

DT 20-NOV-2003 (first entry)

DE *Alloiooccus* otitidis antigenic protein SEQ ID NO:1130.

DE *Alloiooccus* otitidis; antigenic protein; immunogenic; immunisation;
 KW gene therapy; Gram-positive bacterium; infection.

OS *Alloiooccus* otitidis.

PN WO2003048304-A2.

PD 12-JUN-2003.

PF 25-NOV-2002; 2002WO-US036123.

PR 29-NOV-2001; 2001US-0133377P.

PR 18-NOV-2002; 2002US-0426742P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;

DR WPI; 2003-505284/47.

DR N-PSDB; ADB07189.

PT New *Alloiooccus* otitidis polynucleotides and polypeptides, useful for
 PT treating and diagnosing diseases, drug screening assays and monitoring of
 PT effects during drug clinical trials.

PS Claim 33; SEQ ID NO 1130; 1019pp; English.

XX The present invention describes an isolated polynucleotide (I) of
 CC *Alloiooccus* otitidis genomic DNA, which encodes an antigenic protein.
 CC *Alloiooccus* otitidis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an
 CC expression vector comprising the novel isolated polynucleotide (I), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological

CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against *Alloiooccus* otitidis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying *Alloiooccus*
 CC otitidis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (1) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting *Alloiooccus*
 CC otitidis. The present sequence represents an *Alloiooccus* otitidis
 CC antigen protein from the present invention.

SQ Sequence 459 AA;

Query Match 79.6%; Score 39; DB 6; Length 459;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAWG 7
 :|||||
 Db 276 VSRFAWG 282

RESULT 14

ABU21625

ID ABU21625 standard; protein; 746 AA.

XX AC ABU21625;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #7152.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia fungorum.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,

PI Wall D, Trawick JB, Carr GJ, Yamamoto R, Forsyth RA, Xu HH,

XX WPI; 2003-029926/02.

DR N-PSDB; ACA25495.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 49549; 1765pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 746 AA;

Query Match 77.6%; Score 38; DB 6; Length 746;

Best Local Similarity 85.7%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0;

QY 1 ISRFAWG 7

Db 149 LSRFAWG 155
 :|||||

RESULT 15

ADE08590

ID ADE08590 standard; protein; 234 AA.

AC ADE08590;

XX 29-JAN-2004 (first entry)

DE Novel protein (useful for identifying genetic disorders) #745.

XX novel gene; novel protein; tissue marker; molecular weight marker;

KW chromosome marker; Genetic disorder.

XX Unidentified.

XX WO2003054152-A2.

XX 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.

PR 12-APR-2002; 2002US-0372615P.

PR 22-APR-2002; 2002US-00128558.

PR 24-APR-2002; 2002US-0376045P.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

XX WPI; 2003-569235/53.

DR N-PSDB; ADS07679.

XX New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1656; 1177pp; English.

CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.

XX SQ Sequence 234 AA;

Query Match 76.5%; Score 37.5; DB 7; Length 234;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 ISRFAWG-GEV 9

Db 164 VSRFAWVGEV 173
 :|||||

Search completed: November 7, 2005, 11:49:01

Job time : 173 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 11:43:19 ; Search time 43 Seconds
(without alignments)
15.624 Million cell updates/sec

Title: US-09-856-086B-8
Perfect score: 49
Sequence: 1 ISRFAMGEV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	93.9	141	4	US-09-328-352-7227 Sequence 7227, Ap
2	39	79.6	136	4	US-09-489-039A-13925 Sequence 13925, A
3	39	79.6	426	4	US-09-107-532A-4197 Sequence 4197, Ap
4	36	73.5	233	4	US-09-540-236-2317 Sequence 2317, Ap
5	35	71.4	9	3	US-08-159-139A-1078 Sequence 1078, Ap
6	35	71.4	12	2	US-08-735-253-1 Sequence 1, Appli
7	35	71.4	20	2	US-08-468-540B-11 Sequence 11, Appl
8	35	71.4	20	3	US-08-297-395-23 Sequence 23, Appl
9	35	71.4	127	4	US-08-468-996-8 Sequence 8, Appli
10	35	71.4	137	4	US-09-252-991A-32243 Sequence 32243, A
11	35	71.4	167	4	US-08-468-996-7 Sequence 7, Appli
12	35	71.4	168	4	US-08-468-996-6 Sequence 6, Appli
13	35	71.4	168	6	5194425-4 Patent No. 5194425
14	35	71.4	168	6	5194425-4 Patent No. 5194425
15	35	71.4	169	4	US-08-468-996-5 Sequence 5, Appli
16	35	71.4	170	1	US-08-327-372-1 Sequence 1, Appli
17	35	71.4	170	2	US-08-327-357A-1 Sequence 1, Appli
18	35	71.4	170	3	US-08-470-397-1 Sequence 1, Appli
19	35	71.4	170	3	US-09-007-520-1 Sequence 1, Appli
20	35	71.4	170	3	US-08-462-351-3 Sequence 3, Appli
21	35	71.4	170	3	US-09-055-263-1 Sequence 1, Appli
22	35	71.4	170	3	US-09-007-520-1 Sequence 1, Appli
23	35	71.4	170	3	US-08-342-408B-2 Sequence 2, Appli
24	35	71.4	170	4	US-09-602-807-3 Sequence 3, Appli
25	35	71.4	170	4	US-08-468-996-4 Sequence 4, Appli
26	35	71.4	170	6	5194425-3 Patent No. 5194425
27	35	71.4	170	6	5468481-3 Patent No. 5468481

28	35	71.4	170	6	5194425-3 Patent No. 5194425
29	35	71.4	170	6	5468481-3 Patent No. 5468481
30	35	71.4	171	2	US-08-781-122-2 Sequence 2, Appli
31	35	71.4	171	3	US-09-137-759-2 Sequence 2, Appli
32	35	71.4	171	3	US-08-953-937-2 Sequence 2, Appli
33	35	71.4	171	3	US-09-378-244-2 Sequence 2, Appli
34	35	71.4	171	4	US-09-989-476-2 Sequence 2, Appli
35	35	71.4	171	4	US-10-270-707-2 Sequence 2, Appli
36	35	71.4	197	4	US-09-512-563C-54 Sequence 54, Appl
37	35	71.4	429	4	US-09-489-039A-8684 Sequence 8684, Ap
38	35	71.4	448	4	US-09-198-452A-326 Sequence 326, App
39	35	71.4	461	4	US-09-438-185A-311 Sequence 311, App
40	34	69.4	10	2	US-08-735-253-6 Sequence 6, Appli
41	34	69.4	41	2	US-08-735-253-7 Sequence 7, Appli
42	34	69.4	11	2	US-08-735-253-12 Sequence 12, Appl
43	34	69.4	118	2	US-08-888-497-40 Sequence 40, Appl
44	34	69.4	118	3	US-09-097-094-5 Sequence 5, Appli
45	34	69.4	118	3	US-09-362-230-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-09-328-352-7227
; Sequence 7227, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7227
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7227

Query Match 93.9%; Score 46; DB 4; Length 141;
Best Local Similarity 88.9%; Pred. No. 0.58;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISRFAMGEV 9
Db 45 ISRYAMGEV 53
|||||

RESULT 2

US-09-489-039A-13925
; Sequence 13925, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13925
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13925

Query Match 79.6%; Score 39; DB 4; Length 136;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1  ISRFANG 8
      |:|:|:|:|
Db      48  ITRYAWGE 55

RESULT 3
US-09-107-532A-4197
; Sequence 4197 Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...426
; SEQUENCE DESCRIPTION: SEQ ID NO: 4197:
US-09-107-532A-4197

Query Match 79.6%; Score 39; DB 4; Length 426;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  ISRFANG 7
      |:|:|:|:|
Db      241 VSRFANG 247

RESULT 4
US-09-540-236-2317
; Sequence 2317 Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
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; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2317
; LENGTH: 233
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2317

Query Match 73.5%; Score 36; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1  ISRFANG 8
      |:|:|:|:|
Db      196 IARLAWGE 203

RESULT 5
US-08-159-339A-1078
; Sequence 1078, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1078:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1078

Query Match 71.4%; Score 35; DB 3; Length 9;
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Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 2 LSRFSWG 8

RESULT 6

US-08-735-253-1
; Sequence 1, Application US/08735253
; Patent No. 5942491
; GENERAL INFORMATION:
; APPLICANT: Root-Bernstein, Robert S.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Arthritis
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Goldsmith, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,253
; FILING DATE:

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5942491thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: MIC3302P0010US
; TELEPHONE: (312) 616-5400
; TELEFAX: (312) 616-5460

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-735-253-1

Query Match 71.4%; Score 35; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.6;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 2 LSRFSWG 8

RESULT 7

US-08-468-540B-11
; Sequence 11, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue

; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-11

Query Match 71.4%; Score 35; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 7.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 1 LSRFSWG 7

RESULT 8

US-08-297-395-23
; Sequence 23, Application US/08297395A
; Patent No. 6039947
; GENERAL INFORMATION:
; APPLICANT: Howard L. Weiner
; APPLICANT: David A. Hafner
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
; TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
; FILE REFERENCE: 1010/05723US3
; CURRENT APPLICATION NUMBER: US/08/297,395A
; CURRENT FILING DATE: 1994-08-11
; EARLIER APPLICATION NUMBER: 08/059,189
; EARLIER FILING DATE: 1993-05-06
; EARLIER APPLICATION NUMBER: 07/502,559
; EARLIER FILING DATE: 1990-03-30
; EARLIER APPLICATION NUMBER: PCT/US88/02139
; EARLIER FILING DATE: 1988-06-24
; EARLIER APPLICATION NUMBER: 07/065,734
; EARLIER FILING DATE: 1987-06-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-297-395-23

Query Match 71.4%; Score 35; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 7.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 1 LSRFSWG 7

RESULT 9
US-08-468-996-8
; Sequence 8, Application US/08468996
; Patent No. 6645504
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Zheng, Zheng
; APPLICANT: Ahmad, Al-Sabbagh
; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION
; FILE REFERENCE: 1010/16959-US3
; CURRENT APPLICATION NUMBER: US/08/468,996
; PRIOR FILING DATE: 2003-02-07
; PRIOR FILING DATE: 1992-02-28
; PRIOR FILING DATE: 1992-02-28
; PRIOR FILING DATE: 1990-02-21
; PRIOR FILING DATE: 1990-02-21
; PRIOR FILING DATE: 1990-10-15
; PRIOR FILING DATE: 1987-06-24
; PRIOR FILING DATE: 1989-12-20
; PRIOR FILING DATE: 1989-12-20
; PRIOR FILING DATE: 1990-03-02
; PRIOR FILING DATE: 1990-07-10
; PRIOR FILING DATE: 1990-07-10
; PRIOR FILING DATE: 1989-07-14
; PRIOR FILING DATE: 1989-07-14
; PRIOR FILING DATE: 1990-10-31
; PRIOR FILING DATE: 1990-10-31
; PRIOR FILING DATE: 1990-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Rattus sordidus
US-08-468-996-8

Query Match 71.4%; Score 35; DB 4; Length 127;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 108 LSRFSWG 114

RESULT 10
US-09-252-991A-32243
; Sequence 32243, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 32243
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32243

Query Match 71.4%; Score 35; DB 4; Length 137;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 9
Db 45 ITRHAWGDI 53

RESULT 11
US-08-468-996-7
; Sequence 7, Application US/08468996
; Patent No. 6645504
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Zheng, Zheng
; APPLICANT: Ahmad, Al-Sabbagh
; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION
; FILE REFERENCE: 1010/16959-US3
; CURRENT APPLICATION NUMBER: US/08/468,996
; PRIOR FILING DATE: 2003-02-07
; PRIOR FILING DATE: 1992-02-28
; PRIOR FILING DATE: 1992-02-28
; PRIOR FILING DATE: 1990-02-21
; PRIOR FILING DATE: 1990-10-15
; PRIOR FILING DATE: 1987-06-24
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; PRIOR FILING DATE: 1990-07-10
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; PRIOR FILING DATE: 1989-07-14
; PRIOR FILING DATE: 1989-07-14
; PRIOR FILING DATE: 1990-10-31
; PRIOR FILING DATE: 1990-10-31
; PRIOR FILING DATE: 1990-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Cavia porcellus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(166)
; OTHER INFORMATION: where x is unknown or other
US-08-468-996-7

Query Match 71.4%; Score 35; DB 4; Length 167;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 110 LSRFSWG 116

RESULT 12
US-08-468-996-6
; Sequence 6, Application US/08468996

; Patent No. 6645504
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Zheng, Zheng
; APPLICANT: Ahmad, Al-Sabbagh
; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION
; FILE REFERENCE: 1010/16959-US3
; CURRENT APPLICATION NUMBER: US/08/468,996
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 07/843,752
; PRIOR FILING DATE: 1992-02-28
; PRIOR APPLICATION NUMBER: US 07/460,852
; PRIOR FILING DATE: 1990-02-21
; PRIOR APPLICATION NUMBER: US 07/596,936
; PRIOR FILING DATE: 1990-10-15
; PRIOR APPLICATION NUMBER: US 07/065,734
; PRIOR FILING DATE: 1987-06-24
; PRIOR APPLICATION NUMBER: US 07/454,486
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: US 07/487,732
; PRIOR FILING DATE: 1990-03-02
; PRIOR APPLICATION NUMBER: US 07/551,632
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: US 07/379,778
; PRIOR FILING DATE: 1989-07-14
; PRIOR APPLICATION NUMBER: US 07/607,826
; PRIOR FILING DATE: 1990-10-31
; PRIOR APPLICATION NUMBER: US 07/595,468
; PRIOR FILING DATE: 1990-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-08-468-996-6

Query Match 71.4%; Score 35; DB 4; Length 168;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRPAWG 7
:||||:
Db 109 LSRFSWG 115

RESULT 13
5194425-4
; Patent No. 5194425
; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION NUMBER: US 07/460,852
; PRIOR FILING DATE: 1990-02-21
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO: 4;
; LENGTH: 168
5194425-4

Query Match 71.4%; Score 35; DB 6; Length 168;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRPAWG 7
:||||:
Db 109 LSRFSWG 115

RESULT 14
5194425-4
; Patent No. 5194425
; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO: 4;
; LENGTH: 168
5194425-4

Query Match 71.4%; Score 35; DB 6; Length 168;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRPAWG 7
:||||:
Db 109 LSRFSWG 115

RESULT 15
US-08-468-996-5
; Sequence 5, Application US/08468996
; Patent No. 6645504
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Zheng, Zheng
; APPLICANT: Ahmad, Al-Sabbagh
; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION
; FILE REFERENCE: 1010/16959-US3
; CURRENT APPLICATION NUMBER: US/08/468,996
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 07/843,752
; PRIOR FILING DATE: 1992-02-28
; PRIOR APPLICATION NUMBER: US 07/460,852
; PRIOR FILING DATE: 1990-02-21
; PRIOR APPLICATION NUMBER: US 07/596,936
; PRIOR FILING DATE: 1990-10-15
; PRIOR APPLICATION NUMBER: US 07/065,734
; PRIOR FILING DATE: 1987-06-24
; PRIOR APPLICATION NUMBER: US 07/454,486
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: US 07/487,732
; PRIOR FILING DATE: 1990-03-02
; PRIOR APPLICATION NUMBER: US 07/551,632
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: US 07/379,778
; PRIOR FILING DATE: 1989-07-14
; PRIOR APPLICATION NUMBER: US 07/607,826
; PRIOR FILING DATE: 1990-10-31
; PRIOR APPLICATION NUMBER: US 07/595,468
; PRIOR FILING DATE: 1990-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-468-996-5

Query Match 71.4%; Score 35; DB 4; Length 169;
Best Local Similarity 71.4%; Pred. No. 63;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISRPANG 7

Db :|||:|
110 LSRFSWG 116

Search completed: November 7, 2005, 11:53:33
Job time : 44 secs

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OM protein - protein search, using sw model

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Title: US-09-856-086B-8
Perfect score: 49
Sequence: 1 ISRFAMGEV 9

Scoring table: BLOSUM62
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Searched: 1867879 seqs, 418409474 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	49	100.0	9	US-10-889-150-2	Sequence 2, Appli
2	45	91.8	379	US-10-156-761-9245	Sequence 9245, Ap
3	42	85.7	431	US-10-156-761-9506	Sequence 9506, Ap
4	39	79.6	371	US-10-501-282-1126	Sequence 1126, Ap
5	39	79.6	445	US-09-815-242-5010	Sequence 5010, Ap
6	39	79.6	447	US-09-815-242-10908	Sequence 10908, A
7	39	79.6	447	US-10-282-122A-42511	Sequence 42511, A
8	39	79.6	450	US-10-501-282-1128	Sequence 1128, Ap
9	39	79.6	459	US-10-501-282-1130	Sequence 1130, Ap
10	38	77.6	267	US-10-424-599-207893	Sequence 207893,
11	38	77.6	746	US-10-282-122A-49549	Sequence 49549, A

12	37	75.5	656	16	US-10-437-963-106633	Sequence 106633,
13	37	75.5	736	15	US-10-282-122A-49775	Sequence 49775, A
14	36	73.5	62	16	US-10-425-115-18558	Sequence 218558,
15	36	73.5	300	18	US-10-450-763-49882	Sequence 49882, A
16	36	73.5	304	10	US-09-912-976-71	Sequence 53714, A
17	36	73.5	304	10	US-10-005-041A-73	Sequence 71, Appl
18	36	73.5	312	17	US-10-774-355A-2524	Sequence 73, Appl
19	36	73.5	321	15	US-10-005-041A-72	Sequence 2524, Ap
20	36	73.5	321	15	US-10-005-041A-72	Sequence 72, Appl
21	36	73.5	451	14	US-10-216-052-5	Sequence 1804, Ap
22	36	73.5	464	15	US-10-282-122A-44723	Sequence 44723, A
23	35	71.4	9	18	US-10-948-707-561	Sequence 561, App
24	35	71.4	9	18	US-10-889-150-3	Sequence 3, Appli
25	35	71.4	9	20	US-11-031-911-29	Sequence 29, Appl
26	35	71.4	13	18	US-10-948-707-755	Sequence 755, App
27	35	71.4	13	18	US-10-948-707-934	Sequence 934, App
28	35	71.4	127	16	US-10-639-286-8	Sequence 8, Appli
29	35	71.4	138	15	US-10-424-599-177874	Sequence 177874,
30	35	71.4	146	16	US-10-425-115-332835	Sequence 332835,
31	35	71.4	164	15	US-10-282-122A-74468	Sequence 74468, A
32	35	71.4	164	16	US-10-474-782-460	Sequence 460, App
33	35	71.4	167	16	US-10-639-286-7	Sequence 7, Appli
34	35	71.4	168	16	US-10-639-286-6	Sequence 6, Appli
35	35	71.4	169	16	US-10-639-286-5	Sequence 5, Appli
36	35	71.4	169	16	US-10-475-104-32	Sequence 32, Appli
37	35	71.4	169	17	US-10-126-834B-1	Sequence 1, Appli
38	35	71.4	170	13	US-10-015-540-2	Sequence 2, Appli
39	35	71.4	170	14	US-10-199-995-3	Sequence 3, Appli
40	35	71.4	170	14	US-10-639-286-4	Sequence 4, Appli
41	35	71.4	170	18	US-10-773-446-80	Sequence 80, Appli
42	35	71.4	171	8	US-08-484-409-2	Sequence 2, Appli
43	35	71.4	171	9	US-09-989-476-2	Sequence 2, Appli
44	35	71.4	171	9	US-09-947-770-4	Sequence 4, Appli
45	35	71.4	171	9	US-09-947-770-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-889-150-2
; Sequence 2, Application US/10889150
; Publication No. US20050214862A1
; GENERAL INFORMATION:
; APPLICANT: Ebringer, Alan
; TITLE OF INVENTION: DIAGNOSIS OF SPONGIFORM DISEASE
; FILE REFERENCE: 78104.072
; CURRENT APPLICATION NUMBER: US/10/889,150
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 09/646,579
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/269,607
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-10-889-150-2

Query Match 100.0%; Score 49; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
|||||
Db 1 ISRFAMGEV 9

RESULT 2
US-10-156-761-9245
; Sequence 9245, Application US/10156761

```
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9245
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9245
```

```
Query Match 91.8%; Score 45; DB 14; Length 379;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ISRFANGEV 9
   |||:||||:
Db 291 ISRYANGEI 299
```

```
RESULT 3
US-10-156-761-9506
; Sequence 9506, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9506
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9506
```

```
Query Match 85.7%; Score 42; DB 14; Length 431;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ISRFANGEV 9
   |||:||||:
Db 343 ITRYANGEI 351
```

```
RESULT 4
US-10-501-282-1126
; Sequence 1126, Application US/10501282
; Publication No. US20050203280A1
```

```
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1126
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-1126
```

```
Query Match 79.6%; Score 39; DB 18; Length 371;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ISRFANG 7
   |||:||||:
Db 188 VSRFANG 194
```

```
RESULT 5
US-09-815-242-5010
; Sequence 5010, Application US/09815242
; Patent No. US20030061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5010
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-5010
```

Query Match 79.6%; Score 39; DB 9; Length 445;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
Db 262 VSRFAMG 268

RESULT 6

US-09-815-242-10908
; Sequence 10908, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10908
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Enterococcus faecalis

US-09-815-242-10908

Query Match 79.6%; Score 39; DB 9; Length 447;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
Db 262 VSRFAMG 268

RESULT 7

US-10-282-122A-42511
; Sequence 42511, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42511
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Enterococcus faecalis

US-10-282-122A-42511

Query Match 79.6%; Score 39; DB 15; Length 447;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
Db 262 VSRFAMG 268

RESULT 8

US-10-501-282-1128
; Sequence 1128, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCWICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1128
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis

US-10-501-282-1128

Query Match 79.6%; Score 39; DB 18; Length 450;

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Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 267 VSRFANG 273

RESULT 9
US-10-501-282-1130
; Sequence 1130, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFs) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1130
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-1130

Query Match 79.6%; Score 39; DB 18; Length 459;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 276 VSRFANG 282

RESULT 10
US-10-424-599-207893
; Sequence 207893, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207893
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(267)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29754C.1.pap
US-10-424-599-207893

Query Match 77.6%; Score 38; DB 15; Length 267;
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```
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 89 LSRFANG 95

RESULT 11
US-10-282-122A-49549
; Sequence 49549, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49549
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49549

Query Match 77.6%; Score 38; DB 15; Length 746;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
Db 149 LSRFANG 155

RESULT 12
US-10-437-963-106633
; Sequence 106633, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```



```

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106633
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(656)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_1105C.1.pap
; US-10-437-963-106633

Query Match          75.5%; Score 37; DB 16; Length 656;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SRPANGEV 9
DB 527 SRYANGHV 534

RESULT 13
US-10-282-122A-49775
; Sequence 49775, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.03A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09

```

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; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49775
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
; US-10-282-122A-49775

Query Match          75.5%; Score 37; DB 15; Length 736;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ISRFANGV 7
DB 144 MSRFANGV 150

RESULT 14
US-10-425-115-218558
; Sequence 218558, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 218558
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_130919C.1.pap
; US-10-425-115-218558

Query Match          73.5%; Score 36; DB 16; Length 62;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISRFANGEV 9
DB 19 ITRFANGKV 27

RESULT 15
US-10-450-763-49882
; Sequence 49882, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49882
; LENGTH: 300
; TYPE: PRT

```

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(300)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49882
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Query Match      73.5%; Score 36; DB 18; Length 300;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Oy 1 ISRFAMGE 8
    | : |||||
Db 183 ITSFAMGE 190
```

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Search completed: November 7, 2005, 12:06:13
Job time : 165 secs
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OM protein - protein search, using sw model

Run on: November 7, 2005, 11:46:14 ; Search time 487 Seconds
(without alignments)
21.585 Million cell updates/sec

Title: US-09-856-086B-8
Perfect score: 49
Sequence: 1 ISRFAMGEV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	49	100.0	9	16	US-09-269-607B-2
3	49	100.0	9	16	US-09-269-607C-3
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5	49	100.0	9	20	US-09-646-579A-2
6	49	100.0	9	23	US-09-856-086A-8
7	49	100.0	9	23	US-09-856-086B-8
8	49	100.0	9	30	US-10-494-781-2
9	49	100.0	9	34	US-10-889-150-2
10	49	100.0	15	30	US-10-494-781-17
11	46	93.9	141	30	US-10-431-652-7227
12	45	91.8	379	27	US-10-156-761-9245
13	42	85.7	431	27	US-10-156-761-9506
14	39	79.6	136	30	US-10-446-203-13925
15	39	79.6	371	1	PCT-US02-36123-1126
16	39	79.6	371	31	US-10-501-282-1126
17	39	79.6	426	30	US-10-417-884A-4197
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19	39	79.6	445	1	PCT-US02-03987-5010
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22	39	79.6	445	37	US-60-269-308-4719
23	39	79.6	447	1	PCT-US02-03987-10908
24	39	79.6	447	1	PCT-US02-09107B-42511
25	39	79.6	447	23	US-09-815-242-10908
26	39	79.6	447	26	US-10-072-851-10908
27	39	79.6	447	28	US-10-282-122A-42511
28	39	79.6	450	1	PCT-US02-36123-1128
29	39	79.6	450	31	US-10-501-282-1128
30	39	79.6	459	1	PCT-US02-36123-1130
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32	38	77.6	267	30	US-10-424-599-207893
33	38	77.6	746	1	PCT-US02-09107B-49549
34	38	77.6	746	28	US-10-282-122A-49549
35	37.5	76.5	234	1	PCT-US02-39555A-1656
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41	37	75.5	518	25	US-09-978-825-1196
42	37	75.5	518	26	US-10-057-498-1196
43	37	75.5	656	30	US-10-437-963-106633
44	37	75.5	736	1	PCT-US02-09107B-49775
45	37	75.5	736	28	US-10-282-122A-49775

ALIGNMENTS

RESULT 1
US-09-269-607-2
; Sequence 2, Application US/09269607
; GENERAL INFORMATION:
; APPLICANT: Ebringer, Alan
; TITLE OF INVENTION: Diagnosis of spongiform disease
; FILE REFERENCE: IT/N7960
; CURRENT APPLICATION NUMBER: US/09/269,607
; CURRENT FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/GB97/02667
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-09-269-607-2

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ISRFAMGEV 9

RESULT 2
US-09-269-607B-2
; Sequence 2, Application US/09269607B
; GENERAL INFORMATION:
; APPLICANT: EBRINGER, ALAN
; TITLE OF INVENTION: Diagnosis of spongiform disease
; FILE REFERENCE: IT/N7960
; CURRENT APPLICATION NUMBER: US/09/269,607B
; CURRENT FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/GB97/02667
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-09-269-607B-2

Query Match      100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFAMGEV 9
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Db      1 ISRFAMGEV 9

RESULT 3
US-09-269-607C-3
; Sequence 3, Application US/09269607C
; GENERAL INFORMATION:
; APPLICANT: ALAN, EBRINGER
; TITLE OF INVENTION: DIAGNOSIS OF SPONGIFORM DISEASE
; FILE REFERENCE: 78104.038
; CURRENT APPLICATION NUMBER: US/09/269,607C
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: GB9620195.9
; PRIOR FILING DATE: 1996-09-27
; PRIOR APPLICATION NUMBER: PCT/GB97/02667
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-09-269-607C-3

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Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFAMGEV 9
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Db      1 ISRFAMGEV 9

RESULT 4
US-09-646-579-2
; Sequence 2, Application US/09646579
; GENERAL INFORMATION:
; APPLICANT: EBRINGER, ALAN
; TITLE OF INVENTION: DIAGNOSIS OF SPONGIFORM OR DE-MYELINATING DISEASE
; FILE REFERENCE: IT/N10335
; CURRENT APPLICATION NUMBER: US/09/646,579
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: PCT/GB99/00876
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-09-646-579-2

Query Match      100.0%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFAMGEV 9
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Db      1 ISRFAMGEV 9

RESULT 5
US-09-646-579A-2
; Sequence 2, Application US/09646579A
; GENERAL INFORMATION:
; APPLICANT: EBRINGER, ALAN
; TITLE OF INVENTION: DIAGNOSIS OF SPONGIFORM OR DE-MYELINATING DISEASE
; FILE REFERENCE: IT/N10335
; CURRENT APPLICATION NUMBER: US/09/646,579A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: PCT/GB99/00876
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-09-646-579A-2

Query Match      100.0%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFAMGEV 9
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Db      1 ISRFAMGEV 9

RESULT 6
US-09-856-086A-8
; Sequence 8, Application US/09856086A
; GENERAL INFORMATION:
; APPLICANT: EBRINGER, ALAN
; TITLE OF INVENTION: DIAGNOSIS OF DEMYELINATING OR SPONGIFORM DISEASE
; FILE REFERENCE: 78104.040
; CURRENT APPLICATION NUMBER: US/09/856,086A
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-856-086A-8

Query Match      100.0%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFAMGEV 9
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Db 1 ISRFAMGEV 9

RESULT 7

US-09-856-086B-8
; Sequence 8, Application US/09856086B
; GENERAL INFORMATION:
; APPLICANT: EBRINGER, ALAN
; TITLE OF INVENTION: DIAGNOSIS OF DEMYELINATING OR SPONGIFORM DISEASE
; FILE REFERENCE: 78104.072
; CURRENT APPLICATION NUMBER: US/09/856,086B
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-856-086B-8

Query Match 100.0%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
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Db 1 ISRFAMGEV 9

RESULT 8

US-10-494-781-2
; Sequence 2, Application US/10494781
; GENERAL INFORMATION:
; APPLICANT: King's College London
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
; FILE REFERENCE: IT/KE/N13246
; CURRENT APPLICATION NUMBER: US/10/494,781
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: GB 0127000.8
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: GB 0202562.5
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter sp.

US-10-494-781-2

Query Match 100.0%; Score 49; DB 30; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
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Db 1 ISRFAMGEV 9

RESULT 9

US-10-889-150-2
; Sequence 2, Application US/10889150
; GENERAL INFORMATION:
; APPLICANT: Ebringer, Alan
; TITLE OF INVENTION: DIAGNOSIS OF SPONGIFORM DISEASE
; FILE REFERENCE: 78104.072
; CURRENT APPLICATION NUMBER: US/10/889,150
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 09/646,579
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/269,607
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Acinetobacter calcoaceticus
US-10-889-150-2

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
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Db 1 ISRFAMGEV 9

RESULT 10

US-10-494-781-17
; Sequence 17, Application US/10494781
; GENERAL INFORMATION:
; APPLICANT: King's College London
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
; FILE REFERENCE: IT/KE/N13246
; CURRENT APPLICATION NUMBER: US/10/494,781
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: GB 0127000.8
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: GB 0202562.5
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bovine

US-10-494-781-17

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Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9
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Db 4 ISRFAMGEV 12

RESULT 11

US-10-431-652-7227
; Sequence 7227, Application US/10431652
; GENERAL INFORMATION:
; APPLICANT: Breton, Gary L.
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: PATH03-08
; CURRENT APPLICATION NUMBER: US/10/431,652
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US 09/328,352
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,701
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7227
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii

US-10-431-652-7227

Query Match 93.9%; Score 46; DB 30; Length 141;
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Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGEV 9

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Db          45 ISRYANGEV 53
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RESULT 12
US-10-156-761-9245
; Sequence 9245, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9245
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9245

Query Match          91.8%; Score 45; DB 27; Length 379;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
|:|:|:|:|
Db 291 ISRYANGEI 299

RESULT 13
US-10-156-761-9506
; Sequence 9506, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9506
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9506

Query Match          85.7%; Score 42; DB 27; Length 431;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
|:|:|:|:|
Db 343 ITRYANGEI 351

RESULT 14
US-10-446-203-13925
; Sequence 13925, Application US/10446203
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/10/446,203
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/489,039
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13925
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-446-203-13925

Query Match          79.6%; Score 39; DB 30; Length 136;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 8
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Db 48 ITRYANGEV 55

RESULT 15
PCT-US02-36123-1126
; Sequence 1126, Application PC/TUS0236123
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company, and Fletcher, Leah D., McMichael, John C.,
; APPLICANT: Russell, David P., and Zagursky, Robert J.
; TITLE OF INVENTION: Alloiococcus otitidis Open Reading Frames (ORFs) Encoding Polypep
; FILE REFERENCE: Antigen 1
; CURRENT APPLICATION NUMBER: PCT/US02/36123
; CURRENT FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1126
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
PCT-US02-36123-1126

Query Match          79.6%; Score 39; DB 1; Length 371;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
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Db 188 VSRFANG 194

Search completed: November 7, 2005, 12:01:47
Job time : 488 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 11:49:09 ; Search time 91 Seconds
(without alignments)
22.416 Million cell updates/sec

Title: US-09-856-086B-8

Perfect score: 49

Sequence: 1 ISRFAWGEV 9

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Total number of hits satisfying chosen parameters: 979076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	73.5	300	6	US-10-450-763-49882
2	36	73.5	300	6	US-10-450-763-53714
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5	36	73.5	885	8	US-60-659-397-915
6	35	71.4	9	7	US-11-031-911-29
7	35	71.4	20	6	US-10-817-970-7779
8	35	71.4	20	6	US-10-817-970-8992
9	35	71.4	120	6	US-10-703-032-160892
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13	35	71.4	304	7	US-11-033-039-824
14	35	71.4	445	6	US-10-526-324-734
15	35	71.4	455	8	US-60-711-491-86
16	35	71.4	459	5	US-09-201-228B-190
17	35	71.4	663	7	US-11-092-052-2818
18	34	69.4	89	7	US-11-150-804-10419
19	34	69.4	89	6	US-60-579-902A-10419
20	34	69.4	92	6	US-10-703-032-154662
21	34	69.4	118	7	US-11-119-831-5
22	34	69.4	138	6	US-10-390-328A-13887
23	34	69.4	138	8	US-60-659-397-1606
24	34	69.4	182	6	US-10-940-774A-10306
25	34	69.4	200	8	US-60-655-875-165397

26	34	69.4	204	6	US-10-526-324-1357	Sequence 1257, Ap
27	34	69.4	222	8	US-60-655-875-160131	Sequence 160131,
28	34	69.4	231	8	US-60-691-214-4287	Sequence 4287, Ap
29	34	69.4	322	7	US-11-031-175-12207	Sequence 12207, A
30	34	69.4	367	7	US-11-096-568A-16420	Sequence 16420, A
31	34	69.4	414	7	US-11-096-568A-16419	Sequence 16419, A
32	34	69.4	491	6	US-10-467-657-5002	Sequence 5002, Ap
33	34	69.4	491	6	US-10-467-657A-5002	Sequence 5002, Ap
34	34	69.4	497	7	US-11-096-568A-3270	Sequence 3270, Ap
35	34	69.4	497	7	US-11-241-607-33551	Sequence 33551, A
36	34	69.4	570	7	US-11-096-568A-3269	Sequence 3269, Ap
37	34	69.4	570	7	US-11-096-568A-3271	Sequence 3271, Ap
38	34	69.4	570	7	US-11-241-607-33550	Sequence 33550, A
39	34	69.4	600	7	US-11-096-568A-3268	Sequence 3268, Ap
40	34	69.4	600	7	US-11-241-607-33549	Sequence 33549, A
41	34	69.4	640	7	US-11-031-175-13375	Sequence 15375, A
42	34	69.4	800	8	US-60-643-717-6803	Sequence 6803, Ap
43	34	69.4	913	7	US-11-096-568A-30511	Sequence 30511, A
44	34	69.4	1020	7	US-11-096-568A-30510	Sequence 30510, A
45	34	69.4	1023	7	US-11-096-568A-30509	Sequence 30509, A

ALIGNMENTS

RESULT 1
US-10-450-763-49882
; Sequence 49882, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49882
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(300)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49882
Query Match 73.5%; Score 36; DB 6; Length 300;
Best Local Similarity 75.0%; Pred. No. 16+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ISRFAWGE 8
|: |||||
DB 183 ITSFAWGE 190
RESULT 2
US-10-450-763-53714
; Sequence 53714, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217

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; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53714
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-53714

Query Match      73.5%; Score 36; DB 6; Length 300;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 ISRFANGE 8
   : |||||
Db 184 ITSFAWGE 191

RESULT 3
US-10-110-176A-8
; Sequence 8, Application US/10110176A
; GENERAL INFORMATION:
; APPLICANT: POULIOT, Jeffrey
; APPLICANT: NASH, Howard A.
; TITLE OF INVENTION: TYROSINE-DNA PHOSPHODIESTERASES (TDP) AND RELATED POLYPEPTIDES,
; TITLE OF INVENTION: NUCLEIC ACIDS, VECTORS, TDP-PRODUCING HOST CELLS, ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 216478
; CURRENT APPLICATION NUMBER: US/10/110,176A
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/27400
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/157,690
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-110-176A-8

Query Match      73.5%; Score 36; DB 6; Length 451;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 ISRFANGEV 9
   : |||||
Db 378 LSKAAWGEV 386

RESULT 4
US-10-330-773A-258
; Sequence 258, Application US/10330773A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773A
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773A-258

Query Match      73.5%; Score 36; DB 6; Length 879;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
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Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 ISRFANGE 8
   : |||||
Db 828 VTRFRWGE 835

RESULT 5
US-60-659-397-915
; Sequence 915, Application US/60659397
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/659,397
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 915
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-659-397-915

Query Match      73.5%; Score 36; DB 8; Length 885;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 ISRFANGE 8
   : |||||
Db 834 VTRFRWGE 841

RESULT 6
US-11-031-911-29
; Sequence 29, Application US/11031911
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey
; APPLICANT: Tang, Qizhi
; APPLICANT: Masteller, Emma
; TITLE OF INVENTION: Regulatory T Cells Suppress Autoimmunity
; FILE REFERENCE: UCSF04-001-2
; CURRENT APPLICATION NUMBER: US/11/031,911
; CURRENT FILING DATE: 2005-01-08
; PRIOR APPLICATION NUMBER: US 60/535,085
; PRIOR FILING DATE: 2004-01-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-911-29

Query Match      71.4%; Score 35; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 8.9e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
   : |||||
Db 2 LSRFSWG 8

RESULT 7
US-10-817-970-7779
; Sequence 7779, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
```



```
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7779
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-7779

Query Match 71.4%; Score 35; DB 6; Length 20;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
DB 8 LSRFSWG 14
:|||||

RESULT 8
US-10-817-970-8992
; Sequence 8992, Application US/10817970.
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
```

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; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8992
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-8992

Query Match 71.4%; Score 35; DB 6; Length 20;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
DB 8 LSRFSWG 14
:|||||

RESULT 9
US-10-703-032-160892
; Sequence 160892, Application US/10703032
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(S3374)B
; CURRENT APPLICATION NUMBER: US/10/703,032
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/020,338
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 211164
; SEQ ID NO 160892
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_TA_55310.pep
US-10-703-032-160892

Query Match 71.4%; Score 35; DB 6; Length 120;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SRFANG 8
DB 78 SRFWGE 84
:|||||

RESULT 10
PCT-US05-03880-80
; Sequence 80, Application PC/TUS0503880
; GENERAL INFORMATION:
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```
; APPLICANT: INANA, GEORGE
; APPLICANT: McLAREN, MARGARET
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 39532-192229
; CURRENT APPLICATION NUMBER: PCT/US05/03880
; CURRENT FILING DATE: 2005-02-09
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03880-80

Query Match 71.4%; Score 35; DB 1; Length 170;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
:|||||
Db 111 LSRFSWG 117

RESULT 11
US-10-517-666-1
; Sequence 1, Application US/10517666
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Avraham
; TITLE OF INVENTION: ANTIGEN-PRESENTING CELLS FOR NEUROPROTECTION AND NERVE REGENERATION
; FILE REFERENCE: PRON-021 US
; CURRENT APPLICATION NUMBER: US/10/517,666
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/388,296
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: PCT/IL03/00500
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Human
US-10-517-666-1

Query Match 71.4%; Score 35; DB 6; Length 170;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
:|||||
Db 111 LSRFSWG 117

RESULT 12
US-11-090-878-54
; Sequence 54, Application US/11090878
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Methods and Reagents for Identifying Compounds for
; TITLE OF INVENTION: Treating Autoimmune Disorders
; FILE REFERENCE: 98-723-C3
; CURRENT APPLICATION NUMBER: US/11/090,878
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HMBP-21
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US-11-090-878-54

Query Match 71.4%; Score 35; DB 7; Length 197;
Best Local Similarity 71.4%; Pred. No. 18+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
:|||||
Db 138 LSRFSWG 144

RESULT 13
US-11-033-039-824
; Sequence 824, Application US/11033039
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 824
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-824

Query Match 71.4%; Score 35; DB 7; Length 304;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMG 7
:|||||
Db 245 LSRFSWG 251

RESULT 14
US-10-526-324-734
; Sequence 734, Application US/10526324
; GENERAL INFORMATION:
; APPLICANT: Imanaka, Takayuki
; APPLICANT: Atomi, Haruyuki
; TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
; TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 490051.40JUSPC
; CURRENT APPLICATION NUMBER: US/10/526,324
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/JP2003/003597
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP 2002-319011
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2167
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 734
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Thermococcus kodakaraensis KOD1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (414542)..(414542)
; OTHER INFORMATION: n is a or c or g or t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (786890)..(786890)
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; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (786907)..(786907)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (786944)..(786946)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (839139)..(839139)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1128488)..(1128488)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1128499)..(1128499)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1128505)..(1128506)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1128517)..(1128518)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1128539)..(1128540)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1561400)..(1561400)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1561477)..(1561477)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1561545)..(1561545)
; OTHER INFORMATION: n is a o r c o r g o r t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1767941)..(1767941)
; OTHER INFORMATION: n is a o r c o r g o r t.
US-10-526-324-734
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Query Match 71.4%; Score 35; DB 6; Length 445;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 2 SRPACGE 8
Db 370 ARPACQ 376
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```
RESULT 15
US-60-711-491-86
; Sequence 86, Application US/60711491
; GENERAL INFORMATION:
; APPLICANT: Kjaenhammer, Todd
; APPLICANT: Russell, William
; APPLICANT: Altermann, Eric
; TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF
; FILE REFERENCE: 035051/296336
; CURRENT APPLICATION NUMBER: US/60/711,491
; CURRENT FILING DATE: 2005-08-26
; NUMBER OF SEQ ID NOS: 2561
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 86
; LENGTH: 455
; TYPE: PRI
; ORGANISM: Lactobacillus acidophilus
US-60-711-491-86
Query Match 71.4%; Score 35; DB 8; Length 455;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ISRFACG 7
Db 270 VSRFTWG 276
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Search completed: November 7, 2005, 12:03:24
Job time : 92 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 11:42:28 ; Search time 38 Seconds
(without alignments)
22.788 Million cell updates/sec

Title: US-09-856-086B-8
Perfect score: 49
Sequence: 1 ISRFAMGEV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	134	2 B35119	4-carboxymuconolactone
2	45	91.8	373	2 T47115	probable 4-carboxy
3	45	91.8	375	2 T35015	probable 3-oxoadip
4	40	81.6	250	2 E82821	NADH-ubiquinone ox
5	40	81.6	449	2 T29425	4-carboxymuconolac
6	38	77.6	126	2 H75300	probable lactoylgl
7	37	75.5	289	2 S77232	hypothetical prote
8	37	75.5	394	2 I51681	poly(A) polymerase
9	36	73.5	230	1 MNIV16	nonstructural prot
10	36	73.5	230	1 MNIVAS	nonstructural prot
11	36	73.5	230	1 MNIVA6	nonstructural prot
12	36	73.5	230	1 MNIVA7	nonstructural prot
13	36	73.5	230	1 MNIVA8	nonstructural prot
14	36	73.5	230	2 A45575	nonstructural prot
15	36	73.5	272	2 T30305	dnaa protein - Lac
16	36	73.5	393	2 B87548	hypothetical prote
17	36	73.5	451	2 A88641	protein F52C12.1 f
18	36	73.5	455	2 A86625	replication initia
19	36	73.5	465	2 A44498	radial spoke prote
20	35	71.4	128	1 MBPNS	myelin basic prote
21	35	71.4	133	2 D83616	gamma-carboxymucon
22	35	71.4	167	2 A37246	myelin basic prote
23	35	71.4	169	1 MBBOB	myelin basic prote
24	35	71.4	171	1 MBCZB	myelin basic prote
25	35	71.4	171	1 MBPGB	myelin basic prote
26	35	71.4	197	1 MBHUB	myelin basic prote
27	35	71.4	328	1 MBMSB	Golli-myelin basic
28	35	71.4	456	2 F81692	chromosomal replic
29	35	71.4	456	2 D71537	probable replicati

ALIGNMENTS

RESULT 1

B35119
4-carboxymuconolactone decarboxylase (EC 4.1.1.44) - Acinetobacter calcoaceticus
C:Species: Acinetobacter calcoaceticus
C>Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C:Accession: B35119
R:Hartnett, C.; Neidle, E.L.; Ngai, K.L.; Ornston, L.N.
J. Bacteriol. 172, 956-966, 1990
A:Title: DNA sequences of genes encoding Acinetobacter calcoaceticus protocatechuate 3, 4-dioxygenase.
A:Reference number: A35119; MUID:90130333; PMID:2298704
A:Accession: B35119
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <HAR>
A:Cross-references: UNIPROT:P20370; GB:M33798; NID:G141771; PID:G141772
C:Superfamily: 4-carboxymuconolactone decarboxylase
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 100.0%; Score 49; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.057; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

QY 1 ISRFAMGEV 9
|||||||
DB 41 ISRFAMGEV 49

RESULT 2

T47115
probable 4-carboxymuconolactone decarboxylase / 3-oxoadipate enol-lactone hydrolase [im-
probable Streptomyces sp.
C:Species: Streptomyces sp.
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C:Accession: T47115
R:Yang, K.; Iwagami, S.; Davies, J.E.
submitted to the EMBL Data Library, May 1999
A:Description: A protocatechuate catabolic gene cluster cloned from Streptomyces sp. 20
A:Reference number: Z24354
A:Accession: T47115
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-373 <YAN>
A:Cross-references: UNIPROT:O9XD79; EMBL:AF109386; PID:AA040815.1
A:Experimental source: strain 2065
C:Genetics:
A:Gene: pcal

Query Match 91.8%; Score 45; DB 2; Length 373;
Best Local Similarity 77.8%; Pred. No. 0.89; 0; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 2

QY 1 ISRFAMGEV 9

```
Db      288 ISRYAWGEI 296
||||:||||:
RESULT 3
T35015
probable 3-oxoadipate enol-lactone hydrolase / 4-carboxymuconolactone decarboxylase - St
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35015
R:Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21565
A:Accession: T35015
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-375 <SEE>
A:Cross-references: UNIPROT:Q9XAM3; EMBL:AL079355; PIDN:CAB45571.1; GSPDB:GN00070; SCOE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: pcaL; SCOE:SC4C6.07C
Query Match      91.8%; Score 45; DB 2; Length 375;
Best Local Similarity 77.8%; Pred. No. 0.89;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFWAGEV 9
|||:||||:
LL      286 ISRYAWGEI 294

RESULT 4
E82821
NADH-ubiquinone oxidoreductase, NQO5 subunit XF0307 [imported] - Xylella fastidiosa (str
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C:Accession: E82821
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: E82821
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <SIM>
A:Cross-references: UNIPROT:Q9PGJ3; GB:AE003884; GB:AE003849; NID:g9105127; PIDN:AAF8311
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0307
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30K/AdhJ/NuoC
Query Match      81.6%; Score 40; DB 2; Length 250;
Best Local Similarity 75.0%; Pred. No. 4.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ISRFWAGE 8
:|||||
Db      90 VGRFWAGE 97
```

```
RESULT 5
T29425
4-carboxymuconolactone decarboxylase homolog - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29425
R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z20619
A:Accession: T29425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-449 <PAR>
A:Cross-references: UNIPROT:O86608; EMBL:AL031155; NID:e1313489; PID:e1313496; PIDN:CAA
C:Genetics:
A:Note: SC3A7.07
Query Match      81.6%; Score 40; DB 2; Length 449;
Best Local Similarity 55.6%; Pred. No. 8.9;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFWAGEV 9
:|||||
Db      361 LTRYAWGEI 369

RESULT 6
H75300
probable lactoylglutathione lyase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75300
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <WHI>
A:Cross-references: UNIPROT:Q9RSB7; GB:AE002054; GB:AE000513; NID:g6460010; PIDN:AAF117;
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2208
A:Map position: 1
Query Match      77.6%; Score 38; DB 2; Length 126;
Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 ISRFWAGE 8
:|||||
Db      94 VTRYAWGE 101

RESULT 7
S77232
hypothetical protein sll1348 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77232
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O.K.; Okumura, S.; Shimoto, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasui
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77232
```

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
 A;Residues: 1-289 <KAN>
 A;Cross-references: UNIPROT:P73526; EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAA1756
 C;Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Start codon: GTG

Query Match 75.5%; Score 37; DB 2; Length 289;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 |||||
 Db 73 ISRYANG 79

RESULT 8
 I51681
 poly(A) polymerase - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51681

R;Gebauer, F.; Richter, J.D.
 Mol. Cell. Biol. 15, 1422-1430, 1995
 A;Title: Cloning and characterization of a Xenopus poly(A) polymerase.
 A;Reference number: I51681; MUID:95166227; PMID:7862135

A;Accession: I51681

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-394 <GEB>

A;Cross-references: UNIPROT:P51006; EMBL:U23456; PIDN:AAA64708.1; PID:g7558

C;Genetics:

A;Gene: PAP

C;Superfamily: poly(A) polymerase

Query Match 75.5%; Score 37; DB 2; Length 394;
 Best Local Similarity 55.6%; Pred. No. 28;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
 ::|||:
 Db 376 LAMFANGEI 384

RESULT 9
 MNIV16
 nonstructural protein NS1 - influenza A virus (strain A/duck/Alberta/60/76)
 C;Species: influenza A virus
 C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
 C;Accession: A04092

R;Baez, M.; Zazra, J.J.; Elliott, R.M.; Young, J.F.; Palese, P.

Virolgy 113, 397-402, 1981

A;Title: Nucleotide sequence of the influenza A/duck/Alberta/60/76 virus NS RNA: conserved

A;Reference number: A04092; MUID:81276929; PMID:6927848

A;Accession: A04092

A;Molecule type: Genomic RNA

A;Residues: 1-230 <BAE>

A;Cross-references: UNIPROT:P03501; GB:J02105; GB:M17071; NID:g324783; PIDN:AAA43509.1;

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing

Query Match 73.5%; Score 36; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 |||||
 Db 198 IQRFANG 204

RESULT 10

MNIVAS

nonstructural protein NS1 - influenza A virus (strain A/mallard/Alberta/88/76)

C;Species: influenza A virus

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C;Accession: A32663

R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.

Virolgy 171, 1-9, 1989

A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,

A;Reference number: A32662; MUID:89299445; PMID:2525836

A;Accession: A32663

A;Molecule type: Genomic RNA

A;Residues: 1-230 <TRE>

A;Cross-references: UNIPROT:P13137

C;Genetics:

A;Gene: NS1

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing; nonstructural protein

Query Match 73.5%; Score 36; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 |||||
 Db 198 IQRFANG 204

RESULT 11

MNIVAS6

nonstructural protein NS1 - influenza A virus (strain A/mallard/Alberta/827/88)

C;Species: influenza A virus

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C;Accession: C32663

R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.

Virolgy 171, 1-9, 1989

A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,

A;Reference number: A32662; MUID:89299445; PMID:2525836

A;Accession: C32663

A;Molecule type: Genomic RNA

A;Residues: 1-230 <TRE>

A;Cross-references: UNIPROT:P03501

C;Genetics:

A;Gene: NS1

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing; nonstructural protein

Query Match 73.5%; Score 36; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 |||||
 Db 198 IQRFANG 204

RESULT 12

MNIVAS7

nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/121/79)

C;Species: influenza A virus

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C;Accession: E32663

R;Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.

Virolgy 171, 1-9, 1989

A;Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,

A;Reference number: A32662; MUID:89299445; PMID:2525836

A;Accession: E32663

A;Molecule type: Genomic RNA

A;Residues: 1-230 <TRE>

A;Cross-references: UNIPROT:P13141

C;Genetics:

A:Gene: NS1
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing; nonstructural protein

Query Match 73.5%; Score 36; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 | |||||
 DB 198 IORFANG 204

RESULT 13

MNIVAB

nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/358/79)

C:Species: influenza A virus

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C:Accession: G32663

R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.

Virology 171, 1-9, 1989

A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a

A:Reference number: A32662; MUID:89299445; PMID:2525836

A:Accession: G32663

A:Molecule type: genomic RNA

A:Residues: 1-230 <TRE>

A:Cross-references: UNIPROT:P13143

C:Genetics:

A:Gene: NS1

A:Map position: segment 8

C:Superfamily: influenza virus nonstructural protein NS1

C:Keywords: alternative splicing; nonstructural protein

Query Match 73.5%; Score 36; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 | |||||
 DB 198 IORFANG 204

RESULT 14

A45575

nonstructural protein NS1 - influenza A virus (strain A/Turkey/Wisconsin/68 [HSN9])

C:Species: influenza A virus

C>Date: 22-Apr-1993 #sequence_revision 22-Jul-1994 #text_change 19-May-2000

C:Accession: A45575

R:Perdue, M.L.

Virus Res. 23, 223-240, 1992

A:Title: Naturally occurring NS gene variants in an avian influenza virus isolate.

A:Reference number: A45575; MUID:92327829; PMID:1320795

A:Accession: A45575

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-230 <PER>

A:Cross-references: GB:S39287

A:Note: the authors translated the codon CTG for residue 141 as Gly, CTG for residue 147

A:Note: sequence extracted from NCBI backbone (NCBIN:108102) and modified

C:Superfamily: influenza virus nonstructural protein NS1

Query Match 73.5%; Score 36; DB 2; Length 230;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFANG 7
 | |||||
 DB 198 IORFANG 204

RESULT 15

T30305

dnaA protein - Lactococcus lactis (fragment)

C:Species: Lactococcus lactis

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30305

R:El-Karoui, M.; Ehrlich, D.; Gruss, A.

Proc. Natl. Acad. Sci. U.S.A. 95, 626-631, 1998

A:Title: Identification of the lactococcal exonuclease/recombinase and its modulation b

A:Reference number: Z20817; MUID:98118563; PMID:9435243

A:Accession: T30305

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-272 <ELK>

A:Cross-references: UNIPROT:O54375; EMBL:U76424; NID:G2909712; PID:G2909713; PIDN:AAC12

C:Genetics:

A:Gene: dnaA

C:Superfamily: replication initiation protein dnaA

Query Match 73.5%; Score 36; DB 2; Length 272;

Best Local Similarity 71.4%; Pred. No. 29;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANG 7

: |||: ||

DB 86 VSRFSWG 92

Search completed: November 7, 2005, 11:52:45

Job time : 40 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2005, 11:41:39 ; Search time 175 Seconds
(without alignments)
26.336 Million cell updates/sec

Title: US-09-856-086B-8
Perfect score: 49
Sequence: 1 ISRFAMGEV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	100.0	134	1 DC4C ACIAD	P20370 acinetobact
2	45	91.8	373	2 Q9XD79	Q9xd79 streptomyc
3	45	91.8	375	2 Q9XAN3	Q9xan3 streptomyc
4	45	91.8	379	2 Q82MF4	Q82mf4 streptomyc
5	42	85.7	128	2 Q63P98	Q63p98 burkholderi
6	42	85.7	130	2 Q89IH0	Q89ih0 bradyrhizob
7	42	85.7	131	2 Q8XX67	Q8xx67 ralstonia s
8	42	85.7	431	2 Q82LP2	Q82lp2 streptomyc
9	40	81.6	250	2 Q8PJ42	Q8pj42 xanthomonas
10	40	81.6	250	2 Q87EQ3	Q87eq3 xylella fas
11	40	81.6	250	2 Q9PGJ3	Q9pgj3 xylella fas
12	40	81.6	449	2 Q86608	Q86608 streptomyc
13	39	79.6	148	2 Q71J82	Q71j82 lactobacill
14	39	79.6	250	2 Q8PT74	Q8pt74 xanthomonas
15	39	79.6	447	1 DNAA ENTFA	Q83z5 enterococcu
16	39	79.6	454	2 Q74M34	Q74m34 lactobacill
17	38	77.6	126	2 Q9RSB7	Q9rsb7 deिनococcu
18	38	77.6	150	2 Q7CSA3	Q7csa3 neurospora
19	38	77.6	471	2 Q6C9X4	Q6c9x4 yarrowia li
20	38	77.6	689	2 Q6RK40	Q6rk40 erwinia chr
21	38	77.6	691	2 P94767	P94767 erwinia chr
22	38	77.6	713	2 Q93PY6	Q93py6 pseudomonas
23	37	75.5	289	2 P73S26	P73s26 synecocyst
24	37	75.5	400	1 PAP3 XENLA	P51006 xenopus lae
25	37	75.5	467	2 Q7P259	Q7p259 chromobacte
26	37	75.5	497	2 Q6A6M1	Q6a6m1 propionibac
27	37	75.5	528	2 Q7XGF7	Q7xgf7 oryza sativ
28	37	75.5	1000	2 Q6MTW4	Q6mtw4 bdellovibri
29	36	73.5	122	2 Q8S8I0	Q8s8i0 arabidopsis
30	36	73.5	164	2 Q92J05	Q92j05 streptococc
31	36	73.5	169	2 Q9U5B4	Q9u5b4 caenorhabdi

Query Match 100.0%; Score 49; DB 1; Length 134;

ALIGNMENTS

RESULT 1

ID DC4C ACIAD STANDARD; PRT; 134 AA.

AC P20370; Q6FBL0;

DT 01-FEB-1991 (Rel. 17, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE 4-carboxymuconolactone decarboxylase (EC 4.1.1.44) (CMD).

GN Name=pcac; OrderedLocusNames=ACIADI710;

OS Acinetobacter sp. (Strain ADP1).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Moraxellaceae; Acinetobacter.

OX NCBI_TaxID=62977;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90130333; PubMed=2298704;

RA Hartnett C., Neidite E.L., Ngai K.-L., Ornston L.N.;

RT "DNA sequences of genes encoding Acinetobacter calcoaceticus

RT protocatechuate 3,4-dioxygenase: evidence indicating shuffling of

RT genes and of DNA sequences within genes during their evolutionary

RT divergence";

RL J. Bacteriol. 172:956-966(1990).

RN [2]

RP SEQUENCE FROM N.A.

RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Ozas S.,

RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,

RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;

RT "Unique features revealed by the genome sequence of Acinetobacter sp.

RT ADP1, a versatile and naturally transformation competent bacterium."

RL Nucleic Acids Res. 0:0-0(2004).

CC -!- CATALYTIC ACTIVITY: 2-carboxy-2,5-dihydro-5-oxofuran-2-acetate =

CC 4,5-dihydro-5-oxofuran-2-acetate + CO(2).

CC -!- PATHWAY: Catabolism of protocatechuate to succinate-and acetyl-CoA

CC in the beta-ketoadipate pathway; third step.

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CC EMBL; L05770; AAC37152.1; -

DR EMBL; C8543861; CAG68552.1; -

DR F01R; B35119; B35119.

DR InterPro; IPR003779; CMD.

DR Pfam; PF02627; CMD; 1.

CC Aromatic hydrocarbons catabolism; Complete proteome; Decarboxylase; Lyase.

FT CONFLICT 79 80 MH -> ID (in Ref. 1).

SQ SEQUENCE 134 AA; 15364 MW; DEE1D61BE1C28A60 CRC64;

```

Best Local Similarity 100.0%; Pred. No. 0.23; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 ISRFANGEV 9
Db 41 ISRFANGEV 49

RESULT 2
Q9XD79 ID Q9XD79 PRELIMINARY; PRT; 373 AA.
AC Q9XD79;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 4-carboxymuconolactone decarboxylase/3-oxoadipate enol-lactone
DE hydrolase.
DE
GN Names:pcal;
OS Streptomyces sp. 2065.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=86383;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2065;
RX DOI=10.1128/AEM.66.4.1499-1508.2000;
RA Iwagami S.G., Yang K., Davies J.;
RT "Characterization of the biotechnological acid catabolic gene cluster
RL Appl. Environ. Microbiol. 66:1499-1508 (2000).
DR EMBL; AF109386; AAD40815.1; -
DR PIR; T47115; T47115.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR0003089; AB hydrolase.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Hydrolase.
SQ SEQUENCE 373 AA; 39583 MW; F11D3017D7A524DC CRC64;

Query Match 91.8%; Score 45; DB 2; Length 373;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
Db 288 ISRYANGEI 296

RESULT 3
Q9XAN3 ID Q9XAN3 PRELIMINARY; PRT; 375 AA.
AC Q9XAN3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone
DE decarboxylase.
GN ORFNames=SC4C6.07c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/a17141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

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RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939128; CAB45571.1; -.
DR PIR; T35015; T35015.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR0003089; AB hydrolase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 375 AA; 39873 MW; 67176A9F3B61BECC CRC64;

Query Match 91.8%; Score 45; DB 2; Length 375;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
Db 286 ISRYANGEI 294

RESULT 4
Q82MF4 ID Q82MF4 PRELIMINARY; PRT; 379 AA.
AC Q82MF4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative 3-oxoadipate enol-lactone hydrolase.
GN Name=pcal; OrderedLocNames=SAV1706;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531 (2003).
DR EMBL; AF005027; BAC69417.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR0003089; AB hydrolase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 379 AA; 40270 MW; 1F380DA1FDE544C4 CRC64;

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Query Match 91.8%; Score 45; DB 2; Length 379;
 Best Local Similarity 77.8%; Pred. No. 3.6;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
 |||:|||||
 DB 291 ISRYANGEI 299

RESULT 5

Q63P98 PRELIMINARY; PRT; 128 AA.
 AC Q63P98;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE 4-carboxymuconolactone decarboxylase (EC 4.1.1.44).
 GN Name=pcaC; ORFNames=BPSS0047;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;
 RX PubMed=15377794;
 RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebahia L.M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Cresset B., Davis P., DeShazer D.,
 RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
 RA Songvilail S., Stevens K., Tumapa S., Vesaratchaveit M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
 RT "Genomic plasticity of the causative agent of melioidosis,
 RT Burkholderia pseudomallei.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
 DR EMBL; BX571966; CH37490.1; -;
 KW Lyase.
 SQ SEQUENCE 128 AA; 14397 MW; D90613F968A5AF1 CRC64;

Query Match 85.7%; Score 42; DB 2; Length 128;
 Best Local Similarity 66.7%; Pred. No. 4.5;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
 |||:|||||
 DB 41 ITRYANGEI 49

RESULT 6

Q89IH0 PRELIMINARY; PRT; 130 AA.
 AC Q89IH0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gamma-carboxymuconolactone decarboxylase.
 GN Name=pcaC; OrderedLocusNames=blr5669;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Iidesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Teurouka H., Wada T., Yamada M.,

RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005955; BAC50934.1; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 KW Complete proteome.
 SQ SEQUENCE 130 AA; 14765 MW; 6A7E54F89B392741 CRC64;

Query Match 85.7%; Score 42; DB 2; Length 130;
 Best Local Similarity 66.7%; Pred. No. 4.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
 |||:|||||
 DB 41 ITRYANGEI 49

RESULT 7

Q8XX67 PRELIMINARY; PRT; 131 AA.
 AC Q8XX67;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE PUTATIVE 4-CARBOXYMUCONOLACTONE DECARBOXYLASE PROTEIN (EC
 4.1.1.44).
 GN Name=pcaC; Synonyms=RS01310; OrderedLocusNames=RSC2249;
 OS Ralstonia solanacearum (pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Denange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646069; CAD15956.1; -;
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR PRINTS; PR01415; ANKYRIN.
 KW Complete proteome; Lyase.
 SQ SEQUENCE 131 AA; 14535 MW; 6000DE287A109FB9 CRC64;

Query Match 85.7%; Score 42; DB 2; Length 131;
 Best Local Similarity 66.7%; Pred. No. 4.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFANGEV 9
 |||:|||||
 DB 41 ITRYANGEI 49

RESULT 8

Q82LP2 PRELIMINARY; PRT; 431 AA.
 AC Q82LP2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative 3-oxoadipate enol-lactone hydrolase.
 GN OrderedLocusNames=SAV1968;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.

```

OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005029; BAC69679.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b_hydrolase.
DR InterPro; IPR003089; AB_hydrolase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR Complete proteome; Hydrolase.
SQ SEQUENCE 431 AA; 46011 MW; 9545AC48C58D2C91 CRC64;

Query Match 85.7%; Score 42; DB 2; Length 431;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAWGEV 9
DB 343 ITRYAWGEI 351
|||||

RESULT 9
Q8PJ42 PRELIMINARY; PRT; 250 AA.
AC Q8PJ42;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NADH-ubiquinone oxidoreductase NQO5 subunit.
GN Name=nucC; OrderedLocusNames=XAC2702;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=1204217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Farfa J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;

Query Match 81.6%; Score 40; DB 2; Length 250;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFAWGE 8
DB 90 VGRFAWGE 97
|||||

RESULT 10
Q87EQ3 PRELIMINARY; PRT; 250 AA.
AC Q87EQ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NADH-ubiquinone oxidoreductase NQO5 subunit.
GN Name=nucC; OrderedLocusNames=PD0250;
OS Xylella fastidiosa (strain Temeculal / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
RA Carver H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuranae E.E.,
RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa.";
RL J. Bacteriol. 185:1018-1026(2003).
CC -!- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain (By
CC similarity);
CC -!- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -!- SIMILARITY: Belongs to the complex I 30 kDa subunit family.
CC EMBL; AB012554; AAO28136.1; -.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

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DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR001268; Complex_30K.
 DR InterPro; IPR010218; Nuoc_fam.
 DR Pfam; PF00329; Complex_30kDa; 1.
 DR ProDom; PD001581; Complex_30K; 1.
 DR TIGRFAMs; TIGR01961; Nuoc_fam; 1.
 DR PROSITE; PS00542; COMPLEX1_30K; 1.
 KW Complete proteome; NAD; Oxidoreductase; Quinone; Ubiquinone.
 SQ SEQUENCE 250 AA; 28093 MW; 0E95DD8DF4EDC5E8 CRC64;

Query Match: 81.6%; Score 40; DB 2; Length 250;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFAMGE 8
 : |||||
 DB 90 VGRFAMGE 97

RESULT 11

Q9PGJ3 PRELIMINARY; PRT; 250 AA.
 ID Q9PGJ3
 AC Q9PGJ3
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE NADH-ubiquinone oxidoreductase, NQ05 subunit.
 GN OrderedLocustNames-Xf0307;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9a5c;
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.B., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Peguero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa E.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Teai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa."
 RL Nature 406:151-159(2000).
 CC -!- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
 sulfur (Fe-S) centers, to quinones in the respiratory chain (By
 similarity).
 CC -!- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
 CC -!- SIMILARITY: Belongs to the complex I 30 kDa subunit family.
 CC EMBL; A5003684; AAF83118.1; -;
 DR FIR; E82821; E82821.

DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR010218; Nuoc_fam.
 DR Pfam; PF00329; Complex_30kDa; 1.
 DR ProDom; PD001581; Complex_30K; 1.
 DR TIGRFAMs; TIGR01961; Nuoc_fam; 1.
 DR PROSITE; PS00542; COMPLEX1_30K; 1.
 KW Complete proteome; NAD; Oxidoreductase; Quinone; Ubiquinone.
 SQ SEQUENCE 250 AA; 28081 MW; 2A96C7D0C981F8DB CRC64;

Query Match: 81.6%; Score 40; DB 2; Length 250;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISRFAMGE 8
 : |||||
 DB 90 VGRFAMGE 97

RESULT 12

O86608 PRELIMINARY; PRT; 449 AA.
 ID O86608
 AC O86608
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone
 DE decarboxylase.
 GN ORFNames=SC3A7.07;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL939127; CAA20070.1; -;
 DR FIR; T29425; T29425.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR000073; A/b hydrolase.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00561; Abhydrolase_1; 1.
 DR PRINTS; PR00111; ABHYDROLASE.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 449 AA; 47531 MW; EC74CB1BF3203927 CRC64;

Query Match: 81.6%; Score 40; DB 2; Length 449;
 Best Local Similarity 55.6%; Pred. No. 38;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFAMGE 9
 : |||||
 DB 361 LTRFAMGEI 369

[illegible]

DR HAMAP; MF 00377; -: 1.
 DR InterPro; IPR001957; Bac_DnaA.
 DR InterPro; IPR010921; Trp_repress_rep.
 DR Pfam; PF00308; Bac_DnaA; 1.
 DR PRINTS; PR00051; DNaA.
 DR TIGRFAMs; TIGR00362; DnaA; 1.
 DR PROSITE; PS01008; DNaA; 1.
 KW ATP-binding; Complete proteome; DNA replication; DNA-binding.
 FT NP_BIND 151 158 ATP (Potential).
 SQ SEQUENCE 447 AA, 50409 MW, 72PCA08F6E7590CA CRC64,

Query Match 79.6%; Score 39; DB 1; Length 447;
 Best Local Similarity 85.7%; Pred. No. 58;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISRFPG 7
 :|||||
 Db 262 VSRPFG 268

Search completed: November 7, 2005, 11:52:02
 Job time : 178 secs

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